

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/575,300
Source: TFWP
Date Processed by STIC: 04/24/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/24/2006

PATENT APPLICATION: US/10/575,300

TIME: 16:18:29

Input Set : A:\PCT-US2004-034573.SEQ LISTING.txt

Output Set: N:\CRF4\04242006\J575300.raw

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3 <110> APPLICANT: Bayer HealthCare
4     Institute of Virology, Slovak Academy of Sciences
5     Ebert, Matthias
6     Rocken, Christoph
7     Pastorekova, Silvia
8     Zavada, Jan
9     Pastorek, Jaromir
11 <120> TITLE OF INVENTION: MN/CA IX AND CANCER PROGNOSIS
13 <130> FILE REFERENCE: MST-2390 PCT
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/575,300
C--> 15 <141> CURRENT FILING DATE: 2006-04-12
15 <150> PRIOR APPLICATION NUMBER: 60/568,019
16 <151> PRIOR FILING DATE: 2004-05-04
18 <150> PRIOR APPLICATION NUMBER: 60/511,832
19 <151> PRIOR FILING DATE: 2003-10-16
21 <160> NUMBER OF SEQ ID NOS: 11
23 <170> SOFTWARE: PatentIn version 3.2
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1522
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (13)..(1389)
35 <220> FEATURE:
36 <221> NAME/KEY: mat_peptide
37 <222> LOCATION: (124)..(1389)
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42           -35                      -30                      -25
44 atc ccg gcc cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg      99
45 Ile Pro Ala Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu
46           -20                      -15                      -10
48 ctg ctt ctg atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag      147
49 Leu Leu Leu Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu
50           -5                      -1 1                      5
52 gat tcc ccc ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc      195
53 Asp Ser Pro Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly
54     10                      15                      20
56 gag gag gat ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca      243
57 Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro
58 25                      30                      35                      40

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| | | |
|-----|---|------|
| 60 | ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag | 291 |
| 61 | Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu | |
| 62 | 45 50 55 | |
| 64 | gat cta cct gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag | 339 |
| 65 | Asp Leu Pro Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys | |
| 66 | 60 65 70 | |
| 68 | tta gag gat cta cct act gtt gag gct cct gga gat cct caa gaa ccc | 387 |
| 69 | Leu Glu Asp Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro | |
| 70 | 75 80 85 | |
| 72 | cag aat aat gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg | 435 |
| 73 | Gln Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp | |
| 74 | 90 95 100 | |
| 76 | cgc tat gga ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg | 483 |
| 77 | Arg Tyr Gly Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala | |
| 78 | 105 110 115 120 | |
| 80 | ggc cgc ttc cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc | 531 |
| 81 | Gly Arg Phe Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe | |
| 82 | 125 130 135 | |
| 84 | tgc ccg gcc ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg | 579 |
| 85 | Cys Pro Ala Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro | |
| 86 | 140 145 150 | |
| 88 | ctc cca gaa ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc | 627 |
| 89 | Leu Pro Glu Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr | |
| 90 | 155 160 165 | |
| 92 | ctg cct cct ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg | 675 |
| 93 | Leu Pro Pro Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg | |
| 94 | 170 175 180 | |
| 96 | gct ctg cag ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg | 723 |
| 97 | Ala Leu Gln Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser | |
| 98 | 185 190 195 200 | |
| 100 | gag cac act gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt | 771 |
| 101 | Glu His Thr Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val | |
| 102 | 205 210 215 | |
| 104 | cac ctc agc acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg | 819 |
| 105 | His Leu Ser Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro | |
| 106 | 220 225 230 | |
| 108 | gga ggc ctg gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa | 867 |
| 109 | Gly Gly Leu Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu | |
| 110 | 235 240 245 | |
| 112 | aac agt gcc tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag | 915 |
| 113 | Asn Ser Ala Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu | |
| 114 | 250 255 260 | |
| 116 | gaa ggc tca gag act cag gtc cca gga ctg gac ata tct gca ctc ctg | 963 |
| 117 | Glu Gly Ser Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu | |
| 118 | 265 270 275 280 | |
| 120 | ccc tct gac ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca | 1011 |
| 121 | Pro Ser Asp Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr | |
| 122 | 285 290 295 | |
| 124 | ccg ccc tgt gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg | 1059 |

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125 Pro Pro Cys Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val
126          300          305          310
128 atg ctg agt gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga      1107
129 Met Leu Ser Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly
130          315          320          325
132 cct ggt gac tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg      1155
133 Pro Gly Asp Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu
134          330          335          340
136 aat ggg cga gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt      1203
137 Asn Gly Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser
138 345          350          355          360
140 cct cgg gct gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt      1251
141 Pro Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly
142          365          370          375
144 gac atc cta gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc      1299
145 Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val
146          380          385          390
148 gcg ttc ctt gtg cag atg aga agg cag cac aga agg gga acc aaa ggg      1347
149 Ala Phe Leu Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly
150          395          400          405
152 ggt gtg agc tac cgc cca gca gag gta gcc gag act gga gcc      1389
153 Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
154          410          415          420
156 tagaggctgg atcttgagaga atgtgagaag ccagccagag gcatctgagg gggagccggt      1449
158 aactgtcctg tctgtctcat tatgccactt cttttaact gcccaagaaat tttttaaaat      1509
160 aaatatttat aat      1522
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 459
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
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171          -35          -30          -25
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175          -20          -15          -10
178 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
179 -5          -1 1          5          10
182 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
183          15          20          25
186 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
187          30          35          40
190 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
191          45          50          55
194 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
195 60          65          70          75
198 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
199          80          85          90
202 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
203          95          100          105

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206 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
207      110      115      120
210 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
211      125      130      135
214 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
215 140      145      150      155
218 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
219      160      165      170
222 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
223      175      180      185
226 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
227      190      195      200
230 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
231      205      210      215
234 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
235 220      225      230      235
238 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
239      240      245      250
242 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
243      255      260      265
246 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
247      270      275      280
250 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
251      285      290      295
254 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
255 300      305      310      315
258 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
259      320      325      330
262 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
263      335      340      345
266 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
267      350      355      360
270 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
271      365      370      375
274 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
275 380      385      390      395
278 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
279      400      405      410
282 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
283      415      420

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286 <210> SEQ ID NO: 3
287 <211> LENGTH: 10898
288 <212> TYPE: DNA
289 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
293 <221> NAME/KEY: gene
294 <222> LOCATION: (1)..(10898)
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature

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Input Set : A:\PCT-US2004-034573.SEQ LISTING.txt

Output Set: N:\CRF4\04242006\J575300.raw

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304 ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttgttaaa cagatgcttg      120
306 aaggcagcat gctcgttaag agtcatcacc aatccctaata ctcaagtaat cagggacaca      180
308 aacactgcgg aagggccgag ggtcctctgc ctaggaaaac cagagacctt tgttcacttg      240
310 tttatctgac cttccctcca ctattgtcca tgaccctgcc aaatccccct ctgtgagaaa      300
312 caccaagaa ttatcaataa aaaaataaat ttaaaaaaaaa aatacaaaaa aaaaaaaaaa      360
314 aaaaaaaaaa gacttacgaa tagttattga taaatgaata gctattggta aagccaagta      420
316 aatgatcata ttcaaaaacca gacggccatc atcacagctc aagtctacct gatttgatct      480
318 ctttatcatt gtcattcttt ggattcacta gattagtcac catcctcaaa attctcccc      540
320 aagttctaata tacgttccaa acatttaggg gttacatgaa gcttgaacct actaccttct      600
322 ttgcttttga gccatgagtt gtaggaatga tgagtttaca ccttacatgc tggggattaa      660
324 tttaaacttt acctctaagt cagttgggta gcctttggct tatttttgta gctaattttg      720
326 tagttaatgg atgcactgtg aatcttgcta tgatagtttt cctccacact ttgccactag      780
328 gggtaggtag gtactcagtt ttcagtaatt gcttacctaa gaccctaagc cctatttctc      840
330 ttgtactggc ctttatctgt aatatgggca tatttaatac aatataattt ttggagtttt      900
332 tttgtttgtt tgtttgtttg tttttttgag acggagtctt gcatctgtca tgcccaggct      960
334 ggagtagcag tggtgccatc tcggctcact gcaagctcca cctcccgagt tcacgccatt      1020
336 ttcctgcctc agcctcccga gtagctggga ctacaggcgc ccgccaccat gcccggttaa      1080
338 ttttttgat ttttggtaga gacggggttt caccgtgtta gccagaatgg tctcgatctc      1140
340 ctgacttcgt gatccacccg cctcggcctc ccaaagtctt gggattacag gtgtgagcca      1200
342 ccgcacctgg ccaatttttt gagtctttta aagtaaaaat atgtcttgta agctggtaac      1260
344 tatggtacat ttcccttttat taatgtggtg ctgacggtca tataggttct tttgagtgtg      1320
346 gcatgcatat gctacttttt gcagtccttt cattacattt ttctctcttc atttgaagag      1380
348 catgttatat ctttttagctt cacttggttt aaaagggtct ctcatagacc taacacagtg      1440
350 tcattgttgg taccacttgg atcataagtg gaaaaacagt caagaaattg cacagtaata      1500
352 cttgtttgta agagggatga ttcaggtgaa tctgacacta agaaactccc ctacctgagg      1560
354 tctgagattc ctctgacatt gctgtatata ggcttttctt ttgacagcct gtgactgcgg      1620
356 actatttttc ttaagcaaga tatgctaag ttttgtgagc ctttttccag agagaggtct      1680
358 catactgca tcaagtgaga acataaatg tctgcattgt tccatatttc aggaatgttt      1740
360 gcttgtgttt tatgtcttta tatagacagg gaaactgtt cctcagtgac ccaaaagagg      1800
362 tgggaattgt tattggatat catcattggc ccacgctttc tgaccttggg aacaattaaag      1860
364 gggtcataat ctcaattctg tcagaattgg tacaagaaat agctgctatg tttcttgaca      1920
W--> 366 ttccacttgg taggaaataa gaatgtgaaa ctcttcagtt ggtgtgtgtc cctngttttt      1980
368 ttgcaatttc cttcttactg tgttaaaaaa aagtatgata ttgctctgag aggtgaggca      2040
370 ttcttaataca tgatctttta agatcaataa tataatcctt tcaaggatta tgtctttatt      2100
372 ataataaaga taatttgtct ttaacagaat caataatata atcccttaaa ggattatatc      2160
374 tttgctgggc gcagtggctc acacctgtaa tcccagcact ttgggtggcc aaggtggaag      2220
376 gatcaaatat gcctacttct atattatctt ctaaagcaga attcatctct cttccctcaa      2280
378 tatgatgata ttgacagggt ttgccctcac tcaactagatt gtgagctcct gctcagggca      2340
380 ggtagcgttt tttgtttttg tttttgtttt tcttttttga gacagggtct tgctctgtca      2400
382 cccaggccag agtgcaatgg tacagtctca gctcactgca gcctcaaccg cctcggtca      2460
384 aaccatcatc ccatttcagc ctctgagta gctgggacta caggcacatg ccattacacc      2520
386 tggctaattt ttttgtatct ctagtagaga cagggtttgg ccatgttgcc cgggctggtc      2580
388 tcgaactcct ggactcaagc aatccacca cctcagcctc ccaaatgag ggaccgtgtc      2640
390 ttattcattt ccattgcctt agtccatagc ccagtgtgtg acctatggtg gtactaaata      2700
392 aatatttgtt gaatgcaata gtaaatagca tttcaggggag caagaactag attaacaaag      2760

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RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1974

VERIFICATION SUMMARY

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Input Set : A:\PCT-US2004-034573.SEQ LISTING.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1920